

This listing of claims will replace all prior versions, and listings, of claims in the application.
Please amend claim 63 and delete claim 66.

63. (Currently Amended) ~~An oligopeptide~~ A polypeptide for use in a fragment complementation system in vitro or in a eukaryotic system, said polypeptide consisting essentially of:

- (1) a first interactor domain ~~an N-terminal β -lactamase fragment,~~
(2) ~~fused to~~ a flexible polypeptide linker, and
(3) ~~an N-terminal β -lactamase fragment~~ a first interactor domain, wherein said N-terminal β -lactamase fragment;

(a) consists of amino acids 26 to 188 up to amino acid 207 of ~~a~~ **the following** β -lactamase sequence ~~with the following numbering convention:~~

His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly
26 30 35 40

Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu
45 50 55

Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys
60 65 70

Val Leu Leu Cys Gly Ala Val Leu Ser Arg Ile Asp Ala Gly Gln Glu
75 80 85

Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr
90 95 100 105

Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu
110 115 120

Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu

125 130 135

Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His
140 145 150
Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu
155 160 165
Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr ~~Met~~Thr Pro Val Ala
170 175 180 185
Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu
190 195 200
Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala
205 210 215
Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp
220 225 230
Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu
235 240 245
Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly
250 255 260 265
Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly
270 275 280
Ala Ser Leu Ile Lys His Trp
285

(SEQ ID NO: ~~227~~);

~~wherein said fragment complementation system is used in vitro or in a
eukaryotic host cell;~~

(b) ~~wherein said N-terminal β -lactamase fragment~~ is able to functionally
reconstitute with a C-terminal β -lactamase enzyme fragment consisting of amino
acids 288 to 208 up to amino acid 189 of said β -lactamase sequence; ~~and~~

~~wherein said N-terminal β -lactamase fragment is altered from said β -lactamase sequence by at least one amino acid substitution selected from the group consisting of:~~

- ~~(a) a lysine to glutamic acid substitution at position 55,~~
- ~~(b) a proline to serine substitution at position 62, and~~
- ~~(c) a methionine to threonine substitution at position 182.~~

64. (Currently Amended) The ~~β -lactamase enzyme fragment~~ polypeptide of claim 63, wherein said N-terminal β -lactamase fragment consists of amino acids 26 to 195 up to amino acid 202 of said β -lactamase sequence.

65. (Currently Amended) The ~~β -lactamase enzyme fragment~~ polypeptide of claim 63, wherein said N-terminal β -lactamase fragment consists of amino acids 26 to 197 of said β -lactamase sequence and said C-terminal β -lactamase fragment consists of amino acids 288 to 198 of said β -lactamase sequence.

66. (Deleted)